BIOGRAPHICAL SKETCH

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NAME: Ruan, Jianbin

eRA COMMONS USER NAME (credential, e.g., agency login): J_RUAN

POSITION TITLE: Assistant Professor of Immunology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Science and Technology of China, Hefei, China	B.S.	07/2007	Biotechnology
University of Science and Technology of China, Hefei, China	Ph.D.	07/2012	Structural Biology
Boston Children's Hospital, Boston, MA	Postdoc	08/2019	Structural Biology and Immunology

A. Personal Statement

My research over the past eight years has been focused on the elucidation of the molecular mechanisms of inflammasome signaling pathways. I am currently the assistant professor in the Department of Immunology at the University of Connecticut Health Center. Our current projects are aiming to elucidate the molecular mechanisms of how non-canonical inflammasome is activated upon sensing its cytosolic ligands, and to elucidate the structural basis of programmed cell deaths that are executed by pore forming proteins including GSDMs, MLKL and NINJ1. For this, we will take a multidisciplinary approach that combines innovative techniques from structural biology, biochemistry and cell biology. My previous research in high-order assemblies in the inflammasome signaling pathways has equipped my lab with unique experiences in this pursuit. My primary expertise lies in biochemistry and structural biology including cryo-electron microscopy and X-ray crystallography. My lab can perform experiments including biochemical and biophysical characterization, biochemical reconstitution, X-ray crystallography, electron microscopy, structure-based mutagenesis, and cellular experiments.

Ongoing and recently completed projects:

R01 AI158435-01
Ruan (PI)
03/17/21-02/28/26
Structural and mechanistic elucidation of non-canonical inflammasome signaling

Charles A. King Trust Postdoctoral Research Fellowship
Ruan (PI)
09/01/17-09/01/19
The killer protein gasdermin D: activation mechanism and a new potential therapeutic target

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2019 – Present	Assistant Professor, Department of Immunology, University of Connecticut Health Center, Farmington, CT
2012 – 2019	Postdoctoral Research Fellow, Program in Cellular and Molecular Medicine, Boston Children's Hospital, Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, MA
2007 – 2012	Graduate Research Assistant, University of Science and Technology of China, Hefei, China
2006 – 2007	Research Assistant, Guangzhou Institute of Biomedicine and Health, Chinese Academy of Sciences, Guangzhou, China

Honors

2017	Charles A. King Trust Postdoctoral Research Fellowship Society
2012	"Zhuliyuehua" Scholarship for Excellent Doctoral Student of Chinese Academy of Sciences
2004	Second Prize of Excellent Undergraduate Scholarship

C. Contributions to Science

1. Elucidating the molecular mechanism of pyroptosis caused by Gasdermins. GSDMD is a recently identified downstream effector of inflammasomes, which are supramolecular complexes that activate inflammatory caspases (-1, 4, 5 and 11). GSDMD contains a functionally important N-terminal domain (GSDMD-NT), a C-terminal domain and a linker in between that is recognized and cleaved by the activated caspases. Upon cleavage, the GSDMD-NT is released and specifically binds to acidic lipids. I unveiled the molecular mechanism of pyroptosis induced by Gasdermin D (GSDMD) using cryo-EM combined with biochemistry and cell biology assays.

   a. Xia S, Zhang Z, Magupalli VG, Pablo JL, Dong Y, Vora SM, Wang L, Fu TM, Jacobson MP, Greka A, Lieberman J, **Ruan J**[#], Wu H[#]. Gasdermin D pore structure reveals preferential release of mature interleukin-1. ***Nature***. 2021 Apr 21;. doi: 10.1038/s41586-021-03478-3. **# Co-corresponding author,** PubMed PMID: 33883744.

   b. **Ruan J**, Xia S, Lieberman J, Wu H. Cryo-EM structure of the Gasdermin A3 membrane pore. ***Nature***. 557:62-7 (2018). PMID: 29695864, PMCID: PMC6007975

   c. Evavold C, **Ruan J**, Tan Y, Xia S, Wu H, Kagan J. The Pore-Forming protein Gasdermin D regulates interleukin-1 secretion from living macrophages. ***Immunity***. 48:35-44 (2018). PMID: 29195811, PMCID: PMC5773350

   d. Liu X[#], Zhang Z[#], **Ruan J**[#], Pan Y, Magupalli VG, Wu H, Lieberman J. Inflammasome-activated gasdermin D causes pyroptosis by forming membrane pores. ***Nature*** 535:153-8 (2016). **# co-first author,** PMID: 27383986, PMCID: PMC5539988

2. Elucidating assembly and activation mechanisms of ASC-dependent inflammasomes. The inflammasome is a multiprotein intracellular complex that detects pathogenic microorganisms and sterile stressors, and that activates the highly pro-inflammatory cytokines interleukin-1β (IL-1β) and IL-18. Addressed the assembly mechanisms for AIM2, NLRPs and NAIP2-NLRC4 inflammasomes using *in vitro* reconstitution, electron microscopy (EM) and polymerization assays. Knowledge of those mechanisms is the key to the development of therapeutic drugs that can target the inflammasomes.

   a. Shen C, Lu A, Xie W, **Ruan J**, Negro R, Egelman E, Fu TM, Wu H. Molecular Mechanism for NLRP6 Inflammasome Assembly and Activation. ***Proceedings of the National Academy of Sciences.*** 116: 2052-7 (2019), PMID: 30674671, PMCID: PMC6369754

   b. Li Y, Fu TM, Lu A, Witt K, **Ruan J**, Shen C, Wu H. Cryo-EM Structures of ASC and NLRC4 CARD Filaments Reveal a Unified Mechanism of Nucleation and Activation of Caspase-1. ***Proceedings of the National Academy of Sciences.*** 115:10845-52 (2018); PMID: 30279182, PMCID: PMC6205419

   c. Zhang L, Chen S, **Ruan J**, Wu J, Tong AB, Yin Q, Li Y, David L, Lu A, Wang WL, Marks C, Ouyang Q, Zhang X, Mao Y, Wu H. Cryo-EM structure of the activated NAIP2-NLRC4

inflammasome reveals nucleated polymerization. ***Science***. 350:404-9 (2015). PMID: 26449474, PMCID: PMC4640189

d. Lu A[#], Magupalli VG[#], **Ruan J[#]**, Yin Q, Atianand MK, Vos MR, Schröder GF, Fitzgerald KA, Wu H, Egelman EH. Unified polymerization mechanism for the assembly of ASC-dependent inflammasomes. ***Cell.*** 156:1193-206 (2014). **# co-first author**, PMID: 24630722, PMCID: PMC4000066

3. Elucidation of selectivity mechanisms of histone modification reader proteins. Post-translational modifications (PTM) of histone proteins are central to the regulation of chromatin structure, playing vital roles in regulating the activation and repression of gene transcription. The actions of PTM to govern DNA transcription are mediated by "readers." I revealed the molecular mechanism of the substrate selectivity by solving the crystal structures of reader proteins Sgf29, Cbx3 and G9a and their complexes with histone peptides harboring different modification states.

   a. Bian C[#], Xu C[#], **Ruan J[#]**, Lee KK[#], Burke TL[#], Tempel W, Barsyte D, Li J, Wu M, Zhou BO, Fleharty BE, Paulson A, Allali-Hassani A, Zhou JQ, Mer G, Grant PA, Workman JL, Zang J, Min J. Sgf29 binds histone H3K4me2/3 and is required for SAGA complex recruitment and histone H3 acetylation. ***The EMBO journal.*** 30:2829-42 (2011). **# co-first author.** PMID: 21685874, PMCID: PMC3160252

   b. **Ruan J[#]**, Ouyang H[#], Amaya MF, Ravichandran M, Loppnau P, Min J, Zang J. Structural basis of the chromodomain of Cbx3 bound to methylated peptides from histone h1 and G9a. ***PloS one***. 7:e35376 (2012). **# co-first author.** PMID: 22514736, PMCID: PMC3325965

   c. **Li** J, Li Z, **Ruan J**, Xu C, Tong Y, Pan PW, Tempel W, Crombet L, Min J, Zang J. Structural basis for specific binding of human MPP8 chromodomain to histone H3 methylated at lysine 9. ***PloS one***. 6:e25104 (2011). PMID: 22022377 PMCID: PMC3192050

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/myncbi/1VOZ7ADHMskQy/bibliography/public/

BIOGRAPHICAL SKETCH

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NAME: **Wang, Chengliang.**
eRA COMMONS USER NAME (credential, e.g., agency login): CHENGLIANG_WANG

POSITION TITLE: **Postdoc of Immunology and Structure Biology**

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE	PERIOD	FIELD OF STUDY
Beijing University of Chemical Technology, Beijing, China	B.S.	09/2006-06/2010	Material Science and Technology
University of Science and Technology of China, Hefei, China	Ph.D.	09/2010-06/2015	Molecular and Structure Biology
University of Science and Technology of China, Hefei, China	Postdoc	07/2015-05/2018	Molecular and Structure Biology
University of Illinois at Urbana-Champaign, IL, USA	Postdoc	05/2018-05/2020	Biochemistry and Structure Biology
University of Connecticut Health Center, CT, USA	Postdoc	05/2020-now	Immunology and Structure Biology

A. Key words of Research Interest:

Immunology; Pyroptosis; Necrosis; Apoptosis; Structure Biology; Macromolecular assemblies; CryoEM; X-ray Crystallography

B. Personal Statement

My research over the past ten years has been focused on the elucidation of the molecular mechanisms of biological process regulation including epigenetics, mitosis, translation and immunity. I am currently working as the postdoc in the Department of Immunology at the University of Connecticut Health Center. My current projects are aiming to elucidate the molecular mechanisms of how non-canonical inflammasome is activated upon sensing its cytosolic ligands, and to elucidate the structural basis of programmed cell deaths that are executed by pore forming proteins including GSDMs, MLKL. For this, we will take a multidisciplinary approach that combines innovative techniques from structural biology, biochemistry and cell biology. My primary expertise lies in biochemistry and structural biology including cryo-electron microscopy and X-ray crystallography, which has equipped myself with unique experiences in this pursuit.

C. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2020 – Present Postdoctoral Research Fellow, Department of Immunology, University of Connecticut Health Center, CT, US
2018 – 2020 Postdoctoral Research Fellow, Department of Biochemistry, University of Illinois at Urbana-Champaign, IL, US
2015 – 2018 Postdoctoral Research Fellow, University of Science and Technology of China, Hefei, China
2006 – 2007 Graduate Research Assistant University of Science and Technology of China, Hefei, China

Honors

2014 “XingYe ZeRen” Scholarship for Excellent Doctoral Student

2013 "Guanghua" Scholarship for Excellent Doctoral Student of Chinese Academy of Sciences
2010 Outstanding Graduate of Beijing

D. Contributions to Science

1. Elucidating the molecular mechanism of kinetochore assembly and function regulation. Kinetochores are large protein networks located on centromeres, which mediate chromosome segregation during mitosis and maintain genomic stability. Mis12 complex (Mis12C) functions as a scaffold that targets Ndc80 and KNL1 complexes to centromere by associating with CENP-C. CENP-A is a variant of histone H3, which specializes the centromere region on chromatin and mediates the kinetochore assembly. The Mis18 complex plays a critical role in initiating the centromere loading of the newly-synthesized CENP-A. Recognition of CENP-A-containing chromatin by CENP-N is a critical step in the assembly of functional kinetochore at the centromere to enable accurate chromosome segregation during cell division. I unveiled the molecular mechanism of kinetochore assembly and regulation using structural biology combined with biochemistry and cell biology assays.

    a. Xing Zhou#, Fan Zheng#, **Chengliang Wang#,** Minhao Wu, Xiaozhen Zhang, Qian Wang, Xuebiao Yao, Chuanhai Fu, Xuan Zhang* and Jianye Zang*, Phosphorylation of CENP-C by Aurora B promotes kinetochore attachment error correction in mitosis. (# represents co-first authorship). ***Proceedings of the National Academy of Sciences***, 114 (50), E10667-E10676

    b. Tian Tian#, Xiaorun Li#, Yingying Liu#, **Chengliang Wang**, Xing Liu, Guoqiang Bi, Xuan Zhang*, Xuebiao Yao*, Z Hong Zhou*, Jianye Zang*, Molecular basis for CENP-N recognition of CENP-A nucleosome on the human kinetochore. (# represents co-first authorship). ***Cell Research***. 28,374-378 (2018)

    c. Min Zhang, Fan Zheng, Yujie Xiong, Chen Shao**, Chengliang Wang**, Minhao Wu, Xiaojia Niu, Fenfen Dong, Xuan Zhang, Chuanhai Fu, Jianye Zang, Centromere targeting of Mis18 requires the interaction with DNA and H2A–H2B in fission yeast. ***Cell. Mol. Life Sci.*** 78, 373–384 (2021).

2. Elucidating the molecular mechanisms of how non-canonical inflammasome is activated upon sensing its cytosolic ligands. Inflammatory caspase sensing of cytosolic lipopolysaccharide (LPS) triggers pyroptosis and the concurrent release of damage-associated molecular patterns (DAMPs). The gasdermin proteins play as the executioners of pyroptosis, a lytic pro-inflammatory type of cell death triggered by sensing cytosolic infections and danger signals. My current work is based on combination of biochemistry and cell assay to uncover the LPS-sensing, downstream DAMP releasing, as well as bacterial antagonism to cytosolic immune surveillance.

    a. **Chengliang Wang,** Jianbin Ruan, Mechanistic insights into gasdermin pore formation and regulation in pyroptosis. ***Journal of Molecular Biology***, (2021):167297

    b. A.J. Russo, S.O. Vasudevan, S.P. Méndez-Huergo, P. Kumari, A. Menoret, S. Duduskar, **C.Wang,** J.M. Pérez Sáez, M.M. Fettis,et al. Intracellular immune sensing promotes inflammation via gasdermin D-driven release of a lectin alarmin. ***Nature Immunology*** 22, 154–165 (2021).

    c. Havira, M.S.; Ta, A.; Kumari, P***.; Wang, C***.; Russo, A.J.; Ruan, J.; Rathinam, V.A.; Vanaja, S.K. Shiga toxin suppresses noncanonical inflammasome responses to cytosolic LPS. ***Science. Immunol***. 2020, 5, eabc0217.

3. Elucidation of selectivity mechanisms of histone modification writer, reader and eraser proteins. Post-translational modifications (PTM) of histone proteins are central to the regulation of chromatin structure, playing vital roles in regulating the activation and repression of gene transcription. The actions of PTM to govern DNA transcription are mediated and regulate by "writer", "reader" and "eraser". Combination using of chemical biochemistry, mass spectrometry, biochemistry and structure biology, I identified and revealed the molecular mechanism of H3K20me3 special reader spindling-1, histone desuccinylation protein sirt5. Besides, I also elucidate the molecular mechanism of protein involved other PTM process.

    a. **Chengliang Wang#**, Minhao Wu#, Li Zhan#, Rongsheng Ma, Jun Yao,Ying Xiong, Yang Pan, Xuan Zhang*, Jianye Zang* Spindlin-1 recognizes methylations of K20 and R23 of histone H4 tail. (# represents co-first authorship). ***FEBS letters*** 592 (24), 4098-4110.

b. T Hang, W Chen, M Wu, L Zhan, **C Wang**, N Jia, X Zhang, J Zang, Structural insights into the molecular mechanism underlying Sirt5-catalyzed desuccinylation of histone peptides, **Biochemical Journal** 476 (2), 211-223,2019

c. **Wang, Chengliang;** Zhang, Qiongdi; Hang, Tianrong; Tao, Yue; Ma, Xukai; Wu, Minhao; Zhang, Xuan; Zang, Jianye, Structure of the JmjC domain-containing protein NO66 complexed with ribosomal protein Rpl8, ***Acta Crystallographica Section D-Biological Crystallography***, 71, pp 1955-1964, 8/2015.

4. Elucidation of the molecular mechanism of fundamental component of Staphylococcal aureus and its infection.
Staphylococcal aureus (*S. aureus*) infection can lead to a wide range of diseases such as sepsis and pneumonia. RNA degradosome is a multiprotein complex regulates the metabolism of RNA, the expression of virulence factors, and the formation of biofilms. Staphylococcal superantigen like (SSL) proteins, specifically expressed by S. aureus, are shown to be involved in immune evasion during S. aureus infection. SdrE functions on the surface of S. aureus for complement evasion. I worked in these multi-process using biochemistry and structure biology to elucidate the molecular mechanism of *S.aureus* infection of humans. Knowledge of those mechanisms is the key to the development of therapeutic drugs that can target the *S.aureus* infection.

a. Nan Jia, Guo Li, Wanbiao Chen, **Chengliang Wang,** Ling Chen, Xiaoling Ma, Xuan Zhang, Yue Tao, Jianye Zang, Xi Mo, Jinfeng Hu. Staphylococcal Superantigen-Like Protein 10 (SSL10) induces necroptosis through TNFR1 activation of RIPK3-dependent signal pathways. DOI: https://doi.org/10.21203/rs.3.rs-445262/v1

b. T. Hang, W. Chen, M. Wu, L. Zhan, **C. Wang**, N. Jia, X. Zhang, J. Zang Structural insights into the molecular mechanism underlying Sirt5-catalyzed desuccinylation of histone peptides. ***Biochemical. Journal****., 476 (2019), pp. 211-223*

c. Tian Tian , **Chengliang Wang** , Minhao Wu, Xuan Zhang , Jianye Zang. Structural Insights into the Regulation of Staphylococcus Aureus Phosphofructokinase by Tetramer-Dimer Conversion, ***Biochemistry***,57(29),4252-4262,2018

d. Yingjie Zhang#, Minhao Wu#, Tianrong Hang#, **Chengliang Wang**, Ye Yang, Weimin Pan, Jianye Zang, Min Zhang, Xuan Zhang. Staphylococcus aureus SdrE captures the factor H C-terminus via a novel "Close, Dock, Lock, and Latch" mechanism for complement evasion. (# represents co-first authorship) ***Biochemical Journal***, 474 (10), pp 1619-1631, 5/2017;

e. Wang Xuejing; **Wang Chengliang;** Wu Minhao; Tian Tian; Cheng Tianyuan; Zhang Xuan; Zang Jianye.Enolase binds to RnpA in competition with PNPase in *Staphylococcus aureus.* ***FEBS Lett***. 591(21):3523-3535,11/2017.

E. Peer-reviewed pubilications:

1. **Chengliang Wang**, Jianbin Ruan, Mechanistic insights into gasdermin pore formation and regulation in pyroptosis. ***Journal of Molecular Biology****, (2021):167297*
2. A.J. Russo, S.O. Vasudevan, S.P. Méndez-Huergo, P. Kumari, A. Menoret, S. Duduskar, **C.Wang**, J.M. Pérez Sáez, M.M. Fettis,et al. Intracellular immune sensing promotes inflammation via gasdermin D–driven release of a lectin alarmin. ***Nature Immunology*** *22, 154–165 (2021).*
3. Min Zhang, Fan Zheng, Yujie Xiong, Chen Shao**, Chengliang Wang**, Minhao Wu, Xiaojia Niu, Fenfen Dong, Xuan Zhang, Chuanhai Fu, Jianye Zang, Centromere targeting of Mis18 requires the interaction with DNA and H2A–H2B in fission yeast. ***Cell. Mol. Life Sci.*** 78, 373–384 (2021).
4. Nan Jia, Guo Li, Wanbiao Chen, **Chengliang Wang,** Ling Chen, Xiaoling Ma, Xuan Zhang, Yue Tao, Jianye Zang, Xi Mo, Jinfeng Hu. Staphylococcal Superantigen-Like Protein 10 (SSL10) induces necroptosis through TNFR1 activation of RIPK3-dependent signal pathways. DOI: https://doi.org/10.21203/rs.3.rs-445262/v1
5. Havira, M.S.; Ta, A.; Kumari, P.; **Wang, C**.; Russo, A.J.; Ruan, J.; Rathinam, V.A.; Vanaja, S.K. Shiga toxin suppresses noncanonical inflammasome responses to cytosolic LPS. ***Science. Immunol****. 2020, 5, eabc0217.*
6. T. Hang, W. Chen, M. Wu, L. Zhan, **C. Wang**, N. Jia, X. Zhang, J. Zang Structural insights into the molecular mechanism underlying Sirt5-catalyzed desuccinylation of histone peptides. ***Biochem. J****., 476 (2019), pp. 211-223*
7. Tian Tian[#], Xiaorun Li[#], Yingying Liu[#], **Chengliang Wang,** Xing Liu, Guoqiang Bi, Xuan Zhang*, Xuebiao Yao*, Z Hong Zhou*, Jianye Zang*, Molecular basis for CENP-N recognition of CENP-A nucleosome on the human kinetochore. (# represents co-first authorship). ***Cell Research.*** 28,374-378 (2018)**.**

8. Xing Zhou[#], Fan Zheng[#], **Chengliang Wang[#]**, Minhao Wu, Xiaozhen Zhang, Qian Wang, Xuebiao Yao, Chuanhai Fu, Xuan Zhang* and Jianye Zang*, Phosphorylation of CENP-C by Aurora B promotes kinetochore attachment error correction in mitosis. (# represents co-first authorship). ***Proc Natl Acad Sci U S A.*** 2017 Dec 12;114(50): E10667-E10676.
9. **Chengliang Wang[#]**, Minhao Wu[#], Li Zhan[#], Rongsheng Ma, Jun Yao,Ying Xiong, Yang Pan, Xuan Zhang*, Jianye Zang* Spindlin-1 recognizes methylations of K20 and R23 of histone H4 tail. (# represents co-first authorship). ***FEBS letters*** 592 (24), 4098-4110
10. **Wang , Chengliang;** Zhang, Qiongdi; Hang, Tianrong; Tao, Yue; Ma, Xukai; Wu, Minhao; Zhang, Xuan; Zang, Jianye, Structure of the JmjC domain-containing protein NO66 complexed with ribosomal protein Rpl8, **Acta Crystallographica Section D-Biological Crystallography**, 71, pp 1955-1964, 8/2015.
11. Tian Tian , **Chengliang Wang** , Minhao Wu, Xuan Zhang , Jianye Zang. Structural Insights into the Regulation of Staphylococcus Aureus Phosphofructokinase by Tetramer-Dimer Conversion, **Biochemistry**,57(29),4252-4262,2018
12. T Hang, W Chen, M Wu, L Zhan, **C Wang**, N Jia, X Zhang, J Zang, Structural insights into the molecular mechanism underlying Sirt5-catalyzed desuccinylation of histone peptides, **Biochemical Journal** 476 (2), 211-223,2019
13. Wang Xuejing; **Wang Chengliang;** Wu Minhao; Tian Tian; Cheng Tianyuan; Zhang Xuan; Zang Jianye.Enolase binds to RnpA in competition with PNPase in *Staphylococcus aureus.* ***FEBS Lett***. 591(21):3523-3535,11/2017.
14. Yingjie Zhang#, Minhao Wu#, Tianrong Hang#, **Chengliang Wang**, Ye Yang, Weimin Pan, Jianye Zang, Min Zhang, Xuan Zhang. Staphylococcus aureus SdrE captures the factor H C-terminus via a novel "Close, Dock, Lock, and Latch" mechanism for complement evasion. (# represents co-first authorship) ***Biochemical Journal***, 474 (10), pp 1619-1631, 5/2017;
15. Weichang Zhang, **Chengliang Wang,** Yang Song, Chen Shao, Xuan Zhang, Jianye Zang, Structural Insights into the Mechanism of Escherichia coli Ymdb: A 2'-O-Acetyl-ADP-ribose Deacetylase, ***Journal of Structural Biology***, 192, 478–486, 10/2015.
16. Yunnfei Wu, **Chengliang Wang**, Shenglong Lin, Minhao Wu, Lu Han, Changlin Tian, Xuan Zhang* and Jianye Zang*, Octameric structure of Staphylococcus aureus enolase in complex with phosphoenolpyruvate, ***Acta Crystallographica Section D-Biological Crystallography*** ,71, pp 2457-2470, 11/2015.
17. Shao, Chen; **Wang, Chengliang;** Zang, Jianye, Structural basis for the substrate selectivity of PvuRts1I, a 5-hydroxymethylcytosine DNA restriction endonuclease, ***Acta Crystallographica Section D-Biological Crystallography***, 70, pp 2477-2486, 2014/9.
18. Sun, Demeng; Liu, Qing; He, Yao; **Wang, Chengliang**; Wu, Fangming; Tian, Changlin; Zang, Jianye, The putative propeptide of MycP1 in mycobacterial type VII secretion system does not inhibit protease activity but improves protein stability., ***Protein & Cell***, 4(12), pp 921-931, 2013/12.
19. Wang, Haipeng; Zhou, Xing; Wu, Minhao; **Wang, Chengliang**; Zhang, Xiaoqin; Tao, Yue; Chen, Nini; Zang, Jianye, Structure of the JmjC-domain-containing protein JMJD5, ***Acta Crystallographica Section D-Biological Crystallography***, 69, pp 1911-1920, 2013/10.
20. Yu, Jigang; **Wang, Chengliang**; Hu, Yanjin; Dong, Yuanqiu; Wang, Ying; Tu, Xiaoming; Peng, Hui; Zhang, Xuecheng, Purification, crystallization and preliminary crystallographic analysis of the marine-amylase AmyP, ***Acta Crystallographica Section F-Biological Crystallography***, 69, pp 263-266, 2013/3.
21. Zhang, Xiaoqin; Chen, Jie; Wu, Minhao; Wu, Huakai; Arokiaraj, Aloysius Wilfred; **Wang, Chengliang**; Zhang, Weichang; Tao, Yue; Huen, Michael S. Y.; Zang, Jianye, Structural basis for role of ring finger protein RNF168 RING domain, ***Cell Cycle***, 12(2), pp 312-321, 2013/1/15.
22. Li, Jing; **Wang, Chengliang**; Wu, Yejuan; Wu, Minhao; Wang, Lin; Wang, Yang; Zang, Jianye, Crystal structure of Sa239 reveals the structural basis for the activation of ribokinase by monovalent cations, ***Journal of Structural Biology***, 177(2), pp 578-582, 2012/2.

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